

## REMARKS

In the September 9, 2006 Office Action, claims 19-22 were rejected as being anticipated by the disclosure in KuberaSampath (U.S. patent 5,674,844). The '844 patent suggests that a broad class of proteins *i.e.*, all morphogens can be used to treat bone loss or increase bone mass in metabolic disease. The '844 patent discloses many potential morphogens. A generic anticipation is, however, not an anticipation. *Eli Lilly v. Zenith Goldline Pharmaceutical*, 05-1396, 1429-1430 (Fed. Cir. Slip. Op. December 26, 2006). Anticipation is a question of fact, including whether or not an element is inherent in the prior art. *See In re Schreiber*, 128 F.3d 1473, 1477 (Fed. Cir. 1997). To anticipate, a prior art reference must place the inventive compound or composition in the possession of the public. *In re Brown*, 329 F.2d 1006, 1011 (C.C.P.A 1964). Thus, the prior art reference must disclose each and every feature of the claimed invention, either explicitly or inherently. *Glaxo Inc. v. Novopharm Ltd.*, 52 F.3d 1043, 1047 (Fed. Cir. 1995). Additionally, the "identical invention must be shown in as complete detail as is contained in the...claim". *Richardson v. Suzuki Motor Co.*, 868 F.2d 1226, 1236 (Fed. Cir. 1989). The '844 claims, however, a measure of what the Applicant, in the '844 patent, was actually in possession of and the specification of the '844 patent specifically state that the morphogen is a dimeric protein. In the presently pending claims, the use of human inhibin A and inhibin B are claimed. Inhibin A and B are not dimeric proteins, rather they are heterodimeric proteins composed of different A and B subunits. This heterodimeric hormone is composed of an inhibin alpha subunit complexed with either an inhibin beta-A subunit, to form inhibin A, or an inhibin beta-B subunit, to form inhibin B. These heterodimeric proteins are not disclosed by KuberaSampath.

Additionally, the data in the '844 application supports a dimeric protein that comprises an amino acid sequence selected from the group consisting of:

- (a) a sequence having at least 70% homology with the C-terminal seven-cysteine skeleton of human OP-1, residues 38-139 of SEQ ID NO: 5, and
- (b) generic Sequence 6, SEQ ID NO: 31;

A sequence alignment of only the seven-cysteine skeleton of the 30-139 sequence, is shown below, comparing BMP7 (OP-1) with the Inhibin alpha subunit and the Activin beta A

subunit which when combined with the Inhibin alpha subunit comprises Inhibin A. This alignment shows that the 70% homology for the 109 aa described by the OP-1 patent is not satisfied.

|             |  | 10 | 20                | 30      | 40  | 50 |
|-------------|--|----|-------------------|---------|-----|----|
|             | 60   | -  |                   |         |     |    |
| BMP7xx0     | CKKHELYVSFRDLGWQDWIIAPEGYAAYCEGECAFPLN---                    |    | SYMNATNHAI        | VQTLVHF |     |    |
| Activin     | CCKQFFVSKDIGWNDWIIAPSGYHANYCEGECPHSIAGTSGSSLSFHSTVINHYRMRG   |    |                   |         |     |    |
| Inhibin     | CHRVALNISFQELGWERWIVYPPSFIFHYCHGGCGLHIP---                   |    | PNLSLPVPGAPPTPAQP |         |     |    |
| Prim. cons. | * : : : * * : * : * . : * * . * : . . : :                    |    |                   |         |     |    |
|             | C3K33L3VSF3DLGW3DWIIAP3GY3A3YCEGEC33HI3GTSGS3LS33333I33T3333 |    |                   |         |     |    |
|             |  | 70 | 80                | 90      | 100 |    |
| BMP7xx0     | INPETVPKPCCAPT--QLNAISVLYFDDS-SNVILKKYRNMVVACGCH             |    |                   |         |     |    |
| Activin     | HSPFANLKS CCVPT--KLRPMMSMLYYDDG-QNIIKKDIQNMIVEECGCS          |    |                   |         |     |    |
| Inhibin     | YSLLPGQAQPCCAALPGTMRPLHVRTTSDGGYSFKYETVPNLLTQHCACI           |    |                   |         |     |    |
| Prim. cons. | . . : . * * .. : . : . * . . . : * : : . . * . *             |    |                   |         |     |    |
|             | 3SP3333KPCCAPTPG3LRP3SVLY3DDGG3N3I3K333NM3V33CGC3            |    |                   |         |     |    |

**Alignment data :**

Alignment length : 109

Identity (\*) : 18 is 16.51 %

Strongly similar (:) : 19 is 17.43 %

Weakly similar (.) : 18 is 16.51 %

Different : 54 is 49.54 %

Sequence 0001 : BMP7xx0 ( 102 residues).

Sequence 0002 : Activin ( 106 residues).

Sequence 0003 : Inhibin ( 105 residues).

Applicant respectfully submits that the '844 patent does not disclose or suggest the claimed invention and that all pending claims are in condition for allowance.

Respectfully Submitted,

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